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--Cells at various times postinfection were harvested and resuspended in ice cold TNE (10 mM Tris [pH 7.8], 150 mM NaCl, 1 mM EDTA) to which NP-40 was then added to a final concentration of 1%. After 5 minutes, the nuclei were pelleted and RNA was extracted from the supernatant using the phenol:chloroform procedure. Equal amounts of total cellular RNA from each sample were then subjected to RT-PCR (Wong, H. et al., (1994) *Anal. Biochem.* 223:251-258) using random hexanucleotide primers (Pharmacia) and RTase (GIBCO-BRL) according to the manufacturers' protocol. The cDNAs from the RT-PCR step were then subjected to selective amplification of reovirus cDNA using appropriate primers that amplify a predicted 116 bp fragment. These primer sequences were derived from the S1 sequence determined previously (Nagata, L. et al., (1984) *Nucleic Acids Res.* 12:8699-8710). The GAPDH primers of Wong, H. et al., (1994) *Anal. Biochem.* 223:251-258 were used to amplify a predicted 306 bp GAPDH fragment which served as a PCR and gel loading control. Selective amplification of the s1 and GAPDH cDNA's was performed using Taq DNA polymerase (GIBCO-BRL) according to the manufacturers' protocol using a Perkin Elmer Gene Amp PCR system 9600. PCR was carried out for 28 cycles with each consisting of a denaturing step for 30 seconds at 97°C, annealing step for 45 seconds at 55°C, and polymerization step for 60 seconds at 72°C. PCR products were analyzed by electrophoresis through an ethidium bromide-impregnated TAE-2% agarose gel and photographed under ultra-violet illumination with Polaroid 57 film.--